

WO 99/64607

PCT/FR99/01343

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LIST OF SEQUENCES

(iii) NUMBER OF SEQUENCES: 4

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 121 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GAATTCCCTG TTGACAATTA ATCATCGAAC TAGTTAACTA GTACGCAGCT TGGCTGCAGG 60
TCGACCTGCA GCCAAGCTTG GGCATACATT CAATCAATTG TTATCTAAGG AAATACTTAC 120
A 121

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 1793 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

20 (ix) CHARACTERISTIC:

- (A) NAME/KEY: CDS
(B) POSITION: 123..1190

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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GAATTCCCTG TTGACAATTA ATCATCGAAC TAGTTAACTA GTACGCAGCT TGGCTGCAGG	60
TCGACCTGCA GCCAAGCTTG GGCATACATT CAATCAATTG TTATCTAAGG AAATACTTAC	120
AT ATG CAG ACA AGA AAA ATC GTC CGG GCA GCC GCC GTA CAG GCC GCC	167
Met Gln Thr Arg Lys Ile Val Arg Ala Ala Ala Val Gln Ala Ala	
1 5 10 15	
TCT CCC AAC TAC GAT CTG GCA ACG GGT GTT GAT AAA ACC ATT GAG CTG	215
Ser Pro Asn Tyr Asp Leu Ala Thr Gly Val Asp Lys Thr Ile Glu Leu	
20 25 30	
GCT CGT CAG GCC CGC GAT GAG GGC TGT GAC CTG ATC GTG TTT GGT GAA	263
Ala Arg Gln Ala Arg Asp Glu Gly Cys Asp Leu Ile Val Phe Gly Glu	
35 40 45	
ACC TGG CTG CCC GCC TAT CCC TTC CAC GTC TGG CTG GGC GCA CCG GCC	311
Thr Trp Leu Pro Gly Tyr Pro Phe His Val Trp Leu Gly Ala Pro Ala	
50 55 60	

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TGG TCG CTG AAA TAC AGT GCC CGC TAC TAT GCC AAC TCG CTC TCG CTG Trp Ser Leu Lys Tyr Ser Ala Arg Tyr Tyr Ala Asn Ser Leu Ser Leu 65 70 75	359
GAC AGT GCA GAG TTT CAA CGC ATT GCC CAG GCC GCA CGG ACC TTG GGT Asp Ser Ala Glu Phe Gln Arg Ile Ala Gln Ala Ala Arg Thr Leu Gly 80 85 90 95	407
ATT TTC ATC GCA CTG GGT TAT AGC GAG CGC AGC GGC GGC AGC CTT TAC Ile Phe Ile Ala Leu Gly Tyr Ser Glu Arg Ser Gly Gly Ser Leu Tyr 100 105 110	455
CTG GGC CAA TGC CTG ATC GAC GAC AAG GGC CAG ATG CTG TGG TCG CGT Leu Gly Gln Cys Leu Ile Asp Asp Lys Gly Gln Met Leu Trp Ser Arg 115 120 125	503
CGC AAA CTC AAA CCT ACA CAT GTT GAG CGC ACC GTG TTT GGT GAA GGT Arg Lys Leu Lys Pro Thr His Val Glu Arg Thr Val Phe Gly Glu Gly 130 135 140	551
TAT GCC CGA GAT CTG ATT GTG TCC GAC ACC GAG CTG GGC CGC GTC GGT Tyr Ala Arg Asp Leu Ile Val Ser Asp Thr Glu Leu Gly Arg Val Gly 145 150 155	599
GCC CTG TGC TGC TGG GAG CAC CTG TCC CCC TTG AGC AAG TAC GCG CTG Ala Leu Cys Cys Trp Glu His Leu Ser Pro Leu Ser Lys Tyr Ala Leu 160 165 170 175	647
TAC TCC CAG CAC GAA GCC ATT CAC ATT GCC GCC TGG CCG TCC TTT TCG Tyr Ser Gln His Glu Ala Ile His Ile Ala Ala Trp Pro Ser Phe Ser 180 185 190	695
CTG TAC AGC GAA CAG GCC CAT GCG CTC AGC GCC AAG GTG AAC ATG GCT Leu Tyr Ser Glu Gln Ala His Ala Leu Ser Ala Lys Val Asn Met Ala 195 200 205	743
GCC TCG CAA ATC TAT TCG GTT GAA GGC CAG TGC TTT ACC ATC GCC GCC Ala Ser Gln Ile Tyr Ser Val Glu Gly Gln Cys Phe Thr Ile Ala Ala 210 215 220	791
AGC AGT GTC GTC ACC CAG GAG ACA CTG GAC ATG CTG GAA GTA GGT GAA Ser Ser Val Val Thr Gln Glu Thr Leu Asp Met Leu Glu Val Gly Glu 225 230 235	839
CAC AAC GCC TCC CTG CTG AAA GTG GGC GGC GGC AGT TCC ATG ATT TTT His Asn Ala Ser Leu Leu Lys Val Gly Gly Ser Ser Met Ile Phe 240 245 250 255	887
GCG CCG GAC GGA CGC ACA TTG GCT CCC TAC CTG CCA CAC GAT GCC GAA Ala Pro Asp Gly Arg Thr Leu Ala Pro Tyr Leu Pro His Asp Ala Glu 260 265 270	935
GGC CTG ATC ATT GCC GAT CTG AAC ATG GAA GAA ATT GCC TTC GCC AAG Gly Leu Ile Ile Ala Asp Leu Asn Met Glu Glu Ile Ala Phe Ala Lys 275 280 285	983
GCG ATC AAC GAC CCT GTG GGC CAC TAC TCC AAA CCC GAG GCC ACC CGT Ala Ile Asn Asp Pro Val Gly His Tyr Ser Lys Pro Glu Ala Thr Arg 290 295 300	1031

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CTG GTA CTG GAC CTG GGG CAC CGT GAG CCC ATG ACT CGG GTG CAT TCC Leu Val Leu Asp Leu Gly His Arg Glu Pro Met Thr Arg Val His Ser 305 310 315	1079
AAA AGC GTG ATC CAG GAA GAA GCT CCC GAG CCG CAC GTG CAA AGT ACG Lys Ser Val Ile Gln Glu Ala Pro Glu Pro His Val Gln Ser Thr 320 325 330 335	1127
GCT GCG CCC GTC GCC GTC AGC CAG ACT CAG GAC TCG GAT ACG CTA CTG Ala Ala Pro Val Ala Val Ser Gln Thr Gln Asp Ser Asp Thr Leu Leu 340 345 350	1175
GTG CAA GAA CCG TCC TGA CCCCCAAAAGA TGACAAGGCC CGGGCAAAC Val Gln Glu Pro Ser 355	1223
GTCGGGTCT TGATTCCCTTC TGCGTCCCGG ATCCACTAGT TCTAGAGTCG ACCTGCAGGC ATGCAAGCTT GGGTCCCACC TGACCCCCATG CCGAACTCAG AAGTGAAACG CCGTAGCGCC GATGGTAGTG TGGGGTCTCC CCATGGAGA GTAGGAACT GCCAGGCATC AAATAAAACG AAACGGCTAG TCGAAAGACT GGGCCTTCG TTTTATCTGT TGTTTGTCCG TGAACGCTCT CCTGAGTAGG ACAAAATCCGC CGGGAGCGGA TTTGAACGTT GCGAACGAAAC GGCCCGGAGG GTGGCGGGCA GGACGCCGC CATAAAACTGC CAGGCATCAA ATTAAGCAGA AGGCCATCCT GACGGATGGC CTTTTTGCCT TTCTACAAAC TCTTCCTGTC GTCATATCTA CAAGCCATCC CCCCACAGAT ACGGTAAACT AGCCTCGTT TTGCATCAGG AAAGCAGCTA TGAACCAACTC CTTAAAAACCC TGGAACACAT TTGGCATTGA TCATAATGCT CAGCACATTG TATGTGCCGA AGACGAACAA CAATTACTCA ATGCCCGCGG	1283 1343 1403 1463 1523 1583 1643 1703 1763 1793

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 35 base pairs
 (B) TYPE: nucleotide
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

- 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CCCCCGACA GCTGTCTTGC TTTCGAATTT CTGCC

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(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleotide

5 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

TTGACGTCAG TAGCTGAACA GGAGGG

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